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Restriction Map of the RSV G Gene

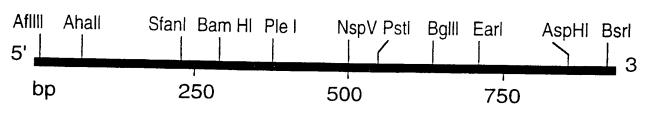


FIG.1

Party (1973) is a firm story party of the control o

FIG.2A

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55	109	163	217	271	325
GAA AAG ACC	AAG TITA AAI	ATC TCA ACT	AAA GTC ACA	ACA ACC CCA	CTG TCT GAA
Glu Lys Thr	Lys Leu Asn	Ile Ser Thr	Lys Val Thr	Thr Thr Pro	Leu Ser Glu
46	100	154	208	262	316
AAG ACA CTA	GGC TTA TAT	GCA ATG ATA	GCA AAC CAC	ATC AAG AAC	TTC TCC AAT (
Lys Thr Leu	Gly Leu Tyr	Ala Met Ile	Ala Asn His	Ile Lys Asn	Phe Ser Asn 1
37	91	145	199	253	307
CGC ACC GCT 7	ATA TCA TCG	TCC ATT CTG	ATA GCC TCG	ACA AGC CAG	GGA ATC AGC
Arg Thr Ala 1	Ile Ser Ser	Ser Ile Leu	Ile Ala Ser	Thr Ser Gln	Gly Ile Ser
28	82	136	190	244	298
AAG GAC CAA	TTA TTA TTC	ATC ACA TTA	ATC ATA TTC	CAA GAT GCA	CCT CAG CTT
Lys Asp Gln	Leu Leu Phe	Ile Thr Leu	Ile Ile Phe	Gln Asp Ala	Pro Gln Leu
19	73	127	181	235	289
TCC AAA AAC	CTC AAT CAT	GTA GCA CAA	ATT ACA GCC	GCA ATC ATA	ACT CAG GAT
Ser Lys Asn	Leu Asn His	Val Ala Gln	Ile Thr Ala	Ala Ile Ile	Thr Gln Asp
10	64	118	172	226	280
TGCAAAC ATG	TGG GAC ACT	CTT AAA TCT	TCA CTT ATA	CTA ACA ACT	ACA TAC CTC
Met	Trp Asp Thr	Leu Lys Ser	Ser Leu Ile	Leu Thr Thr	Thr Tyr Leu

FIG.2B

		3 / 1	9		
379	433	487	541	595	649
GIC AAG TCA	CAA ACA CAA	AAA CCC AAT	TGC AGC AAC	CCA GCA AAG	AAA AAA GAT
Val Lys Ser	Gln Thr Gln	Lys Pro Asn	Cys Ser Asn	Pro Gly Lys	Lys Lys Asp
370	424	478	532	586	640
ACA CCA GGA	ACA ACA ACC	CCA CCA AAC	TGC AGC ATA	AAC AAA AAA	AAG ACA ACC
Thr Pro Gly	Thr Thr Thr	Pro Pro Asn	Cys Ser Ile	Asn Lys Lys	Lys Thr Thr
361	415	469	523	577	631
GCT TCA ACA	AAA AAC ACA	CAA AAC AAA	TTT GTA CCC	AGA ATA CCA	CCA ACC TTC
Ala Ser Thr	Lys Asn Thr	Gln Asn Lys	Phe Val Pro	Arg Ile Pro	Pro Thr Phe
352 ACC AIPA CIPA Thr Ile Leu	406 GTC AAG ACT Val Lys Thr	460 AAA CAA CGC Lys Gln Arg	514 GIG TITT AAC Val Phe Asn	ATC TGC AAA Ile Cys Lys	622 ACA AAA AAA Thr Lys Lys
343 CAA ACC ACC Gln Thr Thr	397 CCC ACA ACA Pro Ithr Ithr	451 CCC ACT ACA Pro I'hr I'hr	505 CAC TTC GAA (His Phe Glu	559 TOC TOG OCT Cys Trp Ala	613 ACC AAG CCT Thr Lys Pro
334	388	442	496	550	604
ATT ACA TCA	AAC CTG CAA (CCC AGC AAG	AAT GAT TTT	AAT CCA ACC	AAA ACC ACC
Ile Thr Ser	Asn Leu Gln)	Pro Ser Lys	Asn Asp Phe	Asn Pro Thr	Lys Thr Thr

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FIG.20

703	_	Glu	
	ACA	Thr	
	\mathcal{L}	Pro	
594	_	Lys 1	
V		Thr 1	
	-	_	
		Thr	
685	22	Pro	
	SIA	Val	
	ZAA.	Glu	
9/9	AG (Lys (
W		Pro I	
	A	Lys	
<i>199</i>	ACT	Thr	
	ACC	Thr	
	CAA	Glu	
658		Pro (
v	Z (A		
	AAA	Lys	
	CIC	Leu	

757	811
C ACC AAC	CTCA ACC
1 Thr Asn	Ser Thr
748	802
ACA CTG CTC	ACC TTC CAC
Thr Leu Leu	Thr Phe His
739	793
HIC ACA ACT	CAA ATG GAA
LIE Thr Thr	Gln Met Glu
730	784
AAA ACA AAC	CTC ACA AGT
Lys Thr Asn	Leu Thr Ser
721	775
AAC ACC ACC	AAT CCA AAA
Asn Thr Thr	Asn Pro Lys
712	766
GAG CCA ACC ATC A	AAC ACC ACA GGA 1
Glu Pro Thr Ile A	ASN Thr Thr Gly 1

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865	GAC CCA	His Pro
856	S	hr Ser
847	IC TCC ACA A	al Ser Thr T
838	CCT TCT CAA G	Thro Ser Gln Val Ser Thr T
829	AAT CTA	Asm Leu Ser
820	TCC GAA GGC	Glu Gly

901 914 CAG TAGITTATTAA AAAAAAA 8 Arg ACA Thr 892 ACA Thr AAC. Pro Asn 22 883 CCA Ser 874 CCC Pro CAA Gln Ser.

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			5 / 1				
54	108	162	216	270	324	378	432
18	36	54	72		108	126	144
CAC AAA GIC ACA CIA ACA ACT GCA AIC AIA CAA GAT GCA ACA AGC CAG AIC AAG	AAC ACA ACC CCA ACA TAC CTC ACT CAG GAT CCT CAG CTT GGA ATC AGC TTC TCC	AAT CTG TCT GAA ATT ACA TCA CAA ACC ACC ACC ATA CTA GCT TCA ACA ACA CCA	OGA GTC AAG TCA AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA ACA	ACC CAA ACA CAA CCC AGC AAG CCC ACT ACA AAA CAA CGC CAA AAC AAA CCA	AAC AAA CCC AAT AAT GAT TIT CAC TIC GAA GIG TITT AAC TITT GIA CCC TGC AGC	ATA TGC AGC AAC AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys	AAA CCA GGA AAG AAA ACC ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA
His Lys Val Thr Leu Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys	AST Thr Thr Pro Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser	Asn Leu Ser Glu Ile Thr Ser Gln Thr Thr Thr Ile Leu Ala Ser Thr Thr Pro	Gly Val Lys Ser Asn Leu Gln Pro Thr Thr Val Lys Thr Lys Asn Thr Thr Thr	Thr Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro	Asn Lys Pro Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser		Liys Pro Gly Liys Liys Thr Thr Thr Liys Pro Thr Liys Liys Pro Thr Phe Liys Thr

FIG.3B

486 162	540 180	594 198	648 216 648	699 232
ACC AAA AAA GAT CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC	AAG CCC ACA GAA GAG CCA ACC ATC AAC ACC ACC AAA ACA AAC ATC ACA ACT ACA	CTG CTC ACC AAC ACC ACA GGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC	TTC CAC TCA ACC TCC TCC GAA GGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA	TOO GAG CAC COA TOA CAA COO TOA TOT COA COO AAO AOA AOA COO CAG TAG
Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr	Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr Thr	Leu Leu Thr Asn Asn Thr Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr	Phe His Ser Thr Ser Ser Glu Gly Asn Leu Ser Pro Ser Gln Val Ser Thr Thr	Ser Glu His Pro Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln .

TTATTAA AAAAAAA

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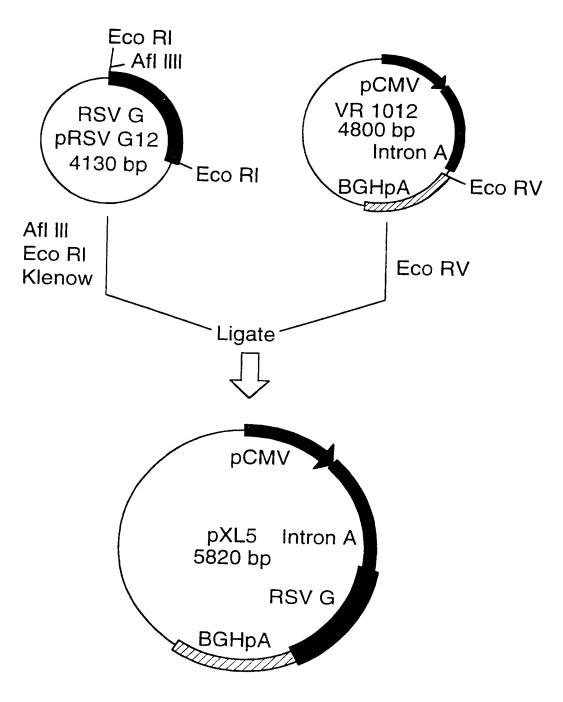


FIG.4.

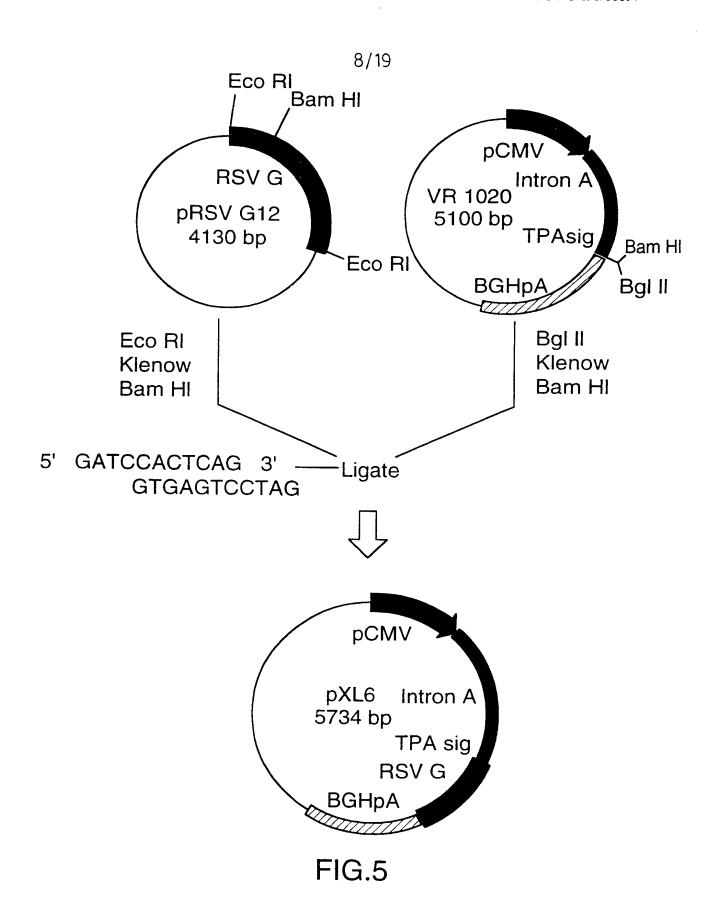


FIG.6A

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70	120 130 140	210	280	350	420	490	560
CAGCITIGIUM	TCAGCGGGTG TTGGCGGGTG TCGGGGCTTGG	CCGCACAGAT	TCATAATATG	TATTAATAGT	CGGTAAATGG	CATAGTAACG	GCAGTACATC
60	130	200	270	340	410	480	550
GAGACGGICA	TTCCCCCCTC	GIGICAAAIA	IGIAICCAIA	AITGACIAGI	ACATAACTTA	CGTATGTTCC	TGCCCACTTG
50 GCAGCICCCG		190 CTGAGAGTGC ACCATATGCG	250 260 270 CTATTGGCA TTGCATACGT TGTATCCATA	330 GACATIGATT	400 GITCCGCGIT	460 470 480 490 CCCATTGACG TCAATAATGA CGTAATGTTCC CATAGTAACG	530 540 550 560 GIGGAGIAIT TACGGIAAAC TCCCCACTIG GCAGIACATC
40 TCTGACACAT	110 TCAGGGCGCG		_	320 CCGCCAIGIT	390 CATATATGGA	460 CCCATTGACG	530 GTGGAGTAIT
30	100	170	240	310	380	450	520
GGTGAAAACC	GACAAGCCCG	GCAGAITIGIA	ATCAGATTGG	TCCAACAITIA	GTTCATAGCC	ACGACCCCC	ACCICAAIGG
10 20 30 40 50 60 70	80 90 100 110	150 160 170	220	290 330 340 320 330 340	360 370 380 390 400 410 ALLOARITAC GGGGICATTA GITCCATAGCC CATATAIGGA GITCCGCGIT ACATAACITA	430 440 450	500 510
TCGCGCGITT CGGIGAIGAC GGIGAAAACC TCTGACACAT GCAGCICCCG GAGACGGICA CAGCITGICT	GIRAGCOGAT GCCOGGAGCA GACAAGCCCG TCAGGGCGC	CITAACIAIG CGGCAICAGA GCAGAITGIA	GCGIPAGGAG AAAAITACCGC AICA	TACAITTATA TIGGCICATG TCCAACAITTA CCGCCAIGIT GACAITGAIT AITGACTAGI		COCCCTGGC TGACCGCCCA ACGACCCCCG	CCAATAGGGA CITICCAITG
10	80	150	220	290	360	430	500
TCGCGCGITIT	GIPAGCGGAT	CITPACIPIG	GCGIPAGGAG	TACAITITAIA	AAICAAIIAC	CCCGCCTGGC	CCAATAGGGA

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FIG.6B

			10 / 1.				
590 600 610 620 630	700	770	840	910	980	1050	1120
CCTA TIGACGICAA IGACGGIAAA IGGCCGCCT GGCAITAIGC	TAITACCAIG	CCAAGICICC	GTCGTAACAA	AGCTCGTTTA	CGGGACCGAT	TAAGTACCOC	GGCCTATAC
620	680 690	750 760	830	890 900 910	970	1040	1110
TGGCCGGCT	ATCTACGTAT TAGTCATCGC	GGITTGACTC ACGGGGATTT	TTTCCAAAAT	TGGGAGGICT ATATAAGCAG AGCTCGTTTA	TAGAAGACAC	AAGAGIGACG	TTTTGGCTTG
610	680	750	820	890	960	1030	1100
TCACCCTAAA	ATCTACGTAT	GGITICACIC	TCAACGGGAAC	TGGGAGGICT	TTGACCTCCA	TCCCGIGCC	GCTATACIGT
600	670	740	810 820 830 840	880	950	1020	1090
TTCACGICAA	TTGGCAGIAC	CGTGGATAGC	GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA	GCGTGTACGG	CCACGCIGIT	GAACCCCCAT	ICITIAIGCAI
ACGCC	660 ACTITICCTAC	730 CATCAATGGG	800 AGTITGITIT	870 TCCCCCTAG	940 GAGACGCCAT	1010 CGGTGCATTG	1080 1090 1100 1110 CCCCTTTIGGC TCTTATGCAT GCTATACTGT TTTTTGGCTTTG
570 580	640 650	710 720 730 740	780 790	860		990 1000 1010 1020	1070
AAGIGIAICA TAIGCCAAGI	CCAGTACATG ACCTTATGGG	GIGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC	ACCCCAITGA CGICAAIGGG	TTGACGCAAA		XYAGCCICCG CGGCCGGAA CGGTGCATTG GAACGCGGAT TCC	FATAGGCACA
570	640	710	780	850 860 870 880	920 930	990	1060 1070
AAGIGIAICA	CCAGTACATG	GIGATGCGGT	ACCCCATTGA	CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGTACGG	GIGAACCGIC AGAICGCCIG	CCAGCCICCG	CTATAGACTC TATAGGCACA
570	640	710	780	850	920	990	1060
AAGIGIATCA	CCAGTACATG	GIGAIGCGGI	ACCCCATTICA	CTCCGCCCCA	GTGAACCGIC	CCAGCCICCG	

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FIG.6C

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			11/19				
1190	1260	1330	1400	1470	1540	1600 1610	1680
ACCAITIAITIG	CAACTATCTC	GGATGGGGTC	ATTAAACATA	CGGCGGAGCT	CICCTAACAG	CACAAGGCCG TGGCGGTAGG	TAAGGCAGCG
1180 1190	1250	1320 1330	1390	1460	1530		1620 1630 1640 1650 1660 1670 1680
TGGGITATTG ACCALTATTG	CTCTTTGCCA	TAITITITACA GGAIGGGGIC	CGCAGITITIT	TCTCCGGTAG	CAGCTCCTTG		GIATGIGICT GAAAATGAGC GTGGAGATTG GGCTCGCACG GCTCACGCAG ATGGAAGACT TAAGGCAGG
1170	1230 1240	1280 1290 1300 1310	1380	1430 1440 1450	1520	1580 1590	1660
CCTATAGGTG	ATTACTAATC CATAACATGG	CAATAC TCTGTCCTTC AGAGACTGAC ACGGACTCTG	CCCCCGIGCC	TCTCGGGTAC GIGTTCCGGA CATGGGCTCT	GETCGCTCGG	CCACCAC CAGIGIGCCG	GCTGACGCAG
1160	1230	1300	1360 1370	1440	1500 1510	G.	1650
TAIPACCITFAG	ATTACTAATC	AGAGACTGAC	CACATATACA ACAACGCGT	GIGITCCGGA	CCATGCCTCC AGGGCTCAT		GGCTCGCACG
1150	1220	1290	1360		1500	1570	1640
TAGGIGATOG	GATACTTTCC	TCTGTCCTTC	CACATATACA		CCATGCCTCC	AGCACAATGC	GTGGAGAITIG
1130 1140 1150	1210	1280	1350	1420	1490	1550 1560 1570 IGGAGGCCAG ACCITAGGCAC AGCACAATGC	1630
ACCCCCCTT CCTTATGCTA TAGGTGATGG	TAITIGGIGAC	ATGCCAATAC	TITIACAAAITI	TCCACGCGAA	AGCCCIGGIC		GAAAAIGAGC
1130	1200	1270	1340	1410	1480	1550	1620
ACCCCCGCTT	ACCACTCCCC TAIT	TATTGGCTAT ATGC	CCAITIAITA TIIBA	GCGIGGGAIC ICCA	TCCACATCCG AGCC	TOCAGOCCAG	GPATGIGICT

FIG.6[

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1750	1820	1890	1960 13	2030	2100	2170	2240
GTTGCGGTGC	GACATAATAG	GTGTGATCA	CAGCCATCTG 6	CCTAATAAAA	3CAGGACAGC	ACCCAGGTGC	ACACACCCTG
1710 1720 1730 1740 1750	1810 1820	1870 1880 1890	1950	2020	2090 2100	2160	2230
CTGAGTIGIT GIATICTGAT AAGAGICAGA GGIAACICCC GITGCGGTGC	CGCGCCACCA GACATAATAG	TOCAGICACC GICGICGACA CGIGIGATICA	TTCTAGITGC	ACTGTCCTTT (GTGGGGTGGG GCAGGACAGC	CTCTATGGGT 7	CITCICIGIG A
1730	1780 1790 1800	1870	1920 1930 1940 1950	2000 2010 2020	2080	2150	2220
AAGAGICAGA	GTAGICTGAG CAGIACTCGT TGCTGCCGCG	TGCAGTCACC	CCAGGCGCCT GGATCCAGAT CTGCTGTGCC TTCTAGTTGC	CCCIGGAAGG IGCCACICCC ACIGICCITI	ATTCTGGGGG	ATGCGGTGGG	GGCACATCCC (
1720	1790	1850 1860	1930	2000	2070 2080	2140	2200 2210
GTATTCTGAT	CAGTACTOGT	TCCTTTCCAT GGGTCTTTTC	GGATCCAGAT	CCCTGGAAGG	GIGICATICT AITICIGGGG	CATGCTGGGG	CTGGGCCA GAAAGAAGCA (
_			1920 CCAGGCGCCT	1990 CCTTCCTTGA	2060 GICIGAGIAG	2130 CAATAGCAGG	2200 TCCTGGGCCA
1690	1770	1840 1840	1910	1970 1980	2040 2050	2120	2180 2190
GCAGAAGAAG ATGCAGGCAG	TGTTAACGGT GGAGGGCAGT	CTGACAGACT AACAGACTGT	CCGCTCTAGA	TIGITIGCCC CICCCCCGIG	TCAGGAAAIT GCAICGCAIT	ATTGGGAAGA	TGAAGAAITG ACCCGGITCC TC
1690	1760	1830	1900	1970	2040	2110 2120	2180
GCAGAAGAAG	TGITAACGGI	CTGACAGACT	GAITAICCCCC	TIGITIGCCC	TCAGGAAATT	AAGGGGGAGG ATTGGGAAGA	TGAAGAATTG

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FIG.6E

	1	3 / 19				
2380	2450	actrac	2590	2660	2730	2800
ACCTAGCCTC	TCCAACAIGT		AGGGGATFAAC	TTCCTCCCCT	GCCGAAACCC	TCCGACCCTG
2370	2440	2510	2580	2650	2720	2790
ACCAAACCAA	AGAAAATGCC	GACTEGETGE	CCACAGAAIC	AAAGGCCGCG	AGTCAGAGGT	GCTCTCCIGT
2360		2500	2570	2640	2710	2740 2750 2760 2770 2780 2790 2800
TCATCAGCCC		CTCGCTCACT	ATACGGITTAT	GGAACCGIAA	TCGACCCTCA	GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG
		2490 CITCCGCITC		2630 CAAAAGGCCA	2700 ATCACAAAAA	2770 CCCTGGAAGC
2340	2410	2480		2620	2690	2760
TGGAGCGGTC	AGCAAGATAG	CATAGAAITIT		AAAAGGCCAG	CCTGACGAGC	AGGCGITITCC
2330	2400	2470	2540	2610	2680	2750
CTAAAGTACT	AAGAAATTAA	TGAGAGAAAT	CGAGCGGTAT	ACATGTGAGC	GCTCCGCCCC	TAAAGATACC
2320	2390	2460	2530	2600	2670	2740
ATCCCACCC	CAAGAGTGGG	GAGGAAGIAA	TCGGCTGCGG	GCAGGAAAGA	TTTTCCATAG	GACAGGACTA
	2330 2340 2350 2360 2370 CTAAAAGTACT TGGAGGGTC TCTCCCTCCC TCATCAGCCC ACCAAACCAA	2340 2350 2360 2370 2380 TGGAGCGGTC TCTCCCTCCC TCATICAGCCC ACCAAACCAA ACCTAGCCTC 2450 2440 2450 AGCAAGATAG GCTAITTAAGT GCAGAGGGAG AGAAAATGCC TCCAACATGT	TGGAGCGGTC TCTCCCTCCC TCATCCAGCCC ACCAAACCAA	2340 2350 2370 TGCAGCGGIC TCTCCCTCCC TCATCAGCCC ACCAAACCAA ACCTAAC 2410 2420 2430 2440 ACCAAACATTAACT ACACAACATTAC TCCACACACCACC TCCAACACAAC TCCAACACAACAAC TCCAACAACAACAACAACAAACAAACAAAACAAAACAA	2340 2350 2360 2370 TOGAGCGGTC TCTCCCTCCC TCATCAGCCC ACCAAACCAA ACCTAAA 2410 2420 2430 2440 TCCAACACAAT AGCAAGAITAG GCAGAGGGAG AGAAAATGC TCCACACACAT TCCAACACAT CAITACAATTT CTTCCCTTCACT CACTCACACATC GCTCACACAATC AGAGGAGAA CAGCTCACTC AAAAGGCCGTTAA ATTACCGTTTAT CCACACACAATC AGAGGAGAA AAAAAGGCCAG AAAAAGGCCGTTAA ATTACTC AAAAAGGCCGCGTTAA AAAAAGGCCGCG TTGCTC	2340 2350 2360 2370 TGGAGCGGTC TCTCCCTCCC TCATCAGCCC ACCAAACCAA ACCTAAC 2410 2420 2430 2440 TCCAAC AGCAAGATTG CCAGAGGGAG AGAAAATGCC TCCAC TCCAAC CATRAGAATTT CTTCCGCTTC CTCCACCACCT CCTCGCTGC CCTCGC CAGCTCCACT AAAGGCGGTA ATACCGTTATT CCACCAGAATC AGGGGGAG CAGCTCCACT AAAGGCGGTA ATACCGGTTATT CCACCAGAATC AGGGGGAG CAGCTCCACT AAAGGCCGGTA ATACCGGTTATT CCACCAGAATC AGGGGGAG AAAAAGGCCAC AAAAGGCCGGAA ATACCGGTTATT AAAAAGGCCAC TTGCTC AAAAAGGCCAG CAAAAAACCCCAC AGAACCCTTAA AAAAAAAACCCAC AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG.6F

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2870	2940	3010	3080 PER 2000 14 / 19	3150	3220	3290	3360
TCACGCTGTA	TTCAGCCCGA	GCCACTGGCA		TTCGGAAA	TTGCAAGCAG	GACGCTCAGT	AGATCCTTTT
2860	2930	3000	3040 3050 3060 3070 3080 $\frac{5}{2}$	3130 3140 3150	3210	3280	3350
TTCTCATAGC TC	GAACCCCCC TI	ACGACTTATC GC		CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA	GITITITIGE ID	TACGGGGTCT GA	ATCTTCACCT AG
2840 2850	2920	2990	3060	3130	3200	3270	
CCTTCGGGAA GCGTGGCGCT	CTGTGTGCAC	CCGGTAAGAC	GCGCTGCTAC	CECTETECTE	GGTAGCGGTG (TGATCITITIC	
	2910	2970 2980	3050	3120	3190	3260	3320 3330 3340
	CCAAGCTGGG	ACTATCGTCT TGAGTCCAAC	AGGTATGTAG	TIGGIAICIG	AACCACCGCT	GAAGATCCTT	GGGAITITIGG TCAIGAGAITF ATCAAAAAGG
2830	2900	2970	3040	3110	3180	3250	3320
CGCCTTTCTC	GTCGITCGCT	ACTAICGICT	TAGCAGAGCG	AGAACAGIAT	CCCCCAAACA	AGGATCTCAA	GGCAITITIGG
2810 2820	2890 2890	2960	3030	3100	3170	3240	3310
COCTITACCE GATACCTETIC	GGTATCTCAG TTCGGTGTAG	TTATCCGGTA	GTAACAGGAT	CTACACTAGA	AGCICTIGAT	GCAGAAAAAA	CTGACGTTAA
2810	2880	2950 2960	3020	3090	3160 3170	3240	3300
CCGCTTACCG	GGTATCTCAG	CCGCTGCGCC TTATCCGGTA	GCAGCCACTG GTAACAGGAT	CIPACTACGG CTACACTAGA	AAGAGITIGGF AGCTCTTGAF	CAGATTACGC GCAGAAAAAA	GGAACGAAAA CTGACGITAA

FIG.6G

			15/19				
3430 TTACCAATGC	3500 CTCGGGGGGG	3570		3710 TCAGCAAAAG	3780 CAACCAATTA	3850 GGATTATCAA	3920 ATAGGATGGC
3420	3490	3560	3640 3610 3620 3630 3640 CACGGTTGAT GAGAGCTTTG TTGTAGGTGG ACCAGTTGGT GATTTTTGAAC	3700	3770	3840	3880 3890 3900 3910 3920
GGICIGACAG	AGITIGCCTGA	GCCTGAATCG		AICCITCAAC	GCCAGIGITA	ATTCATATCA	CETTICIGIA AIGAAGGAGA AAACICACCG AGGCAGITICC ATAGGATGGC
3410	3480	3550	3620	3680 3690 3700 TCGGGAAGAT GCGTGATCTG ATCCTTCAAC	3760	3820 3830	3900
GAGTAAACTT	GITCAICCAI	CTCATACCAG	TTGIAGGIGG		GTAATGCTCT	ATCAAAIGAA ACIGCAAIIIF	AAACTCACCG
3400	3470	3540	3610	3680	3750	3820	3890
AAGTATATAT	TGICTATTIC	GIGITGCIGA	GAGAGCTITIG	TCGGGAAGAT	TCAAGICAGC	ATCAAATGAA	ATGAAGGAGA
3390	3460	3530	3600	3670	3740	3810	3880
AATCAATCTA	CICAGCGAIC	CGTGAAGAAG	CACGGITGAT	GICIGCGITG	caccerccc	CTCATCGAGC	CETTICICIA
3370 3380	3450	3510 3520	3590	3650 3660	3720 3730	3790 3800	3860 3870
AAATTAAAAA TCAAGITTITA	AGGCACCTAT	33333520	GTGAGGGAGC	TITITICETTITE CCACCEAACE	TICGAITTAT ICAACAAAGC	ACCAAITGIG AITAGAAAAA	TACCATATTT TTGAAAAGC
3370	3440 3450	3510	3580 3590	3650	3720	3790	3860
AAATTAAAAA	TTAATCAGTG AGGCACCTAI	GGGGCCCTG	CAGCCAGAAA GIGAGGGAGC	TTTTGCTTTG	TICGAITIPAT	ACCAAITGIG	TACCATAITIT

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3990	4060	4130		4270	4340	4410	4480
CCCCTCGTCA	AAAAGCTTAT	CATCAACCAA		Gaatcaggat	CATCAGGAGT	CAICTCAICT	TTCCCATACA
3980	4050	4120	4190	4260	4330	4400	4470
CTATTAATTT	TGAGAATGGC	AAATCACTCG	TGTTAAAAGG	ATTTTCACCT	AACCATGCAT	TTAGICICAC	CGCATCGGGC '
3960 3970 TCGTCCAACA TCAATACAAC	4040 4020 4030 4040 AAAAIYAAGGI TAICAAGIGA GAAAICACCA IGAGIGACGA CIGAAICCGG	4090 4100 4110 4120 TCAACAGGCC AGCCAITFACG CTCGTCATCA AAATCACTCG	4160 4170 4180 4190 4200 GAGACGAAAT ACGCGATCGC TGTTAAAAGG ACAATTACAA	4250 4260 4270 CATCAACAAT ATTTTCACCT GAATCAGGAT	4320 AGTGGTGAGT	4390 GTCAGCCAGT	
	4030	4100	4170	4230 4240	4310 4320	4380	4450 4460
	TGAGIGACGA	AGCCAITTACG	GAGACGAAAT	GCGCAGGAAC ACTGCCAGCG	CGGGGAICGC AGIGGIGAGI	CATAAATTCC	TGTTTCAGAA ACAACTCTGG
3950	4020	4090	4160	4230	4300	4370	4440
CGAITICCGAC	GAAATCACCA	TCAACAGGCC	GCGCCTGAGC	GCGCAGGAAC	GCIGITITICC	TCGGAAGAGG	ACCITIBCCA
3930 3940	4010	4070 4080	4140 4150	4210 4220	4290	4360	4430
AATATCCIGG TATCGGICIG	TATCAAGTGA	GCAITICITT CCAGACTIGI	ACCGITAITC AITCGIGAIT	ACAGGAATCG AATGCAACCG	TACCTGGAAT	TOCTTGATGG	TGGCAACGCT
3930	4000	4070	4140	4210	4280 4290	4350 4360	4420 4430
AATATCCTGG	AAAATAAGGT	GCAITICITI	ACCGITAITC	ACAGGAATCG	ATTCTTCTAA TACCTGGAAT	ACCCATAAAA TCCTTGATGG	GIAACAICAT IGGCAACGCT

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FIG. 6

	- 4	17	7/19	- A	
4550	4620	4690	4760 5	4830	4900
AATCAGCATC	GTICCITGIA	AIGIAACAIC	GITAITGICI	ATTTCCCCGA	CGTATCACGA
4540	4610	4680	4750	4820	4890
TACCCATATA	GGCTCATAAC	ATCTTGTGCA	ATTTATCAGG	TTCCGCGCAC	Taaaaatagg
4510 4520 4530 4540 4550 GAITIGCCCCA CAITIAICCCC AGCCCAITITA TACCCATATA AAICAGCAIC	4580 4590 4600 4610 4620 GCCICGAGCA AGACGITTICC CGITIGAATAT GCCICATAAC GITICCITIGIA	4650 4660 4670 4680 4690 CAGITITIAIT GITCAIGAIG ATATAITITIT AICTIGIGCA AIGTAACAIC	4720 4730 4740 4750 4760 TOGCTTTCCC CCCCCCCCA TTATTGAAGC ATTTATCAGG GFTATTGTCT	4790 4800 4810 4820 4830 4830 4830 AAIGIAITITA GAAAATAAA CAAATAGGG TICCGCGCAC ATTICCCCGA	4860 4870 4880 4890 4900 AGAAACCAIT AITAICAIGA CAITAACCIA TAAAAATAGG CGIAICACGA
4520	4590	4660	4730	4800	4870
CATTATCGCG	AGACGITICC	GITCAIGAIG	ccccccca	GAAAAATAAA	ATTAICATGA
4510	4580	4650	4720	4790	4860
GATTIGCCCGA	GCCICGAGCA	CAGITITIAIT	TGGCTTTCCC	AATGTATTTA	AGAAACCATT
4500	4570	4640	4710	4770 4780	4840 4850
TGTCGCACCT	TTTAATCGCG	TGTAAGCAGA	agacacaacc	CAIGAGCGGA TACATAITIG	AAAGIGCCAC CIGACGICIA
4490 4500	4560 4570	4630 4640	4700 4710	4770	4840
ATCGATAGAT TGTCGCACCT	CATGITGGAA TITAATCGCG	TTACTGTTTA TGTAAGCAGA	AGAGAITITIG AGACACAACG	CAIGAGCGGA	AAAGTGCCAC

18/19

130

120

110

100

9

80

GGAAAGGGAA GGAGCAAGCC GIGAAITITAA GGGACA

CAGAGCTGAG ATCCTACAGG AGTCCAGGGC TGGAGAGAA ACCTCTGCGA 9 50 30 CTGCAGTCAC CGTCGTCGAC 20

CTCTGCTGTG TGCTGCTGCT GTGTGCAGCA GTCTTCGTTT CGCCCAGC 180 170 160 150

19/19

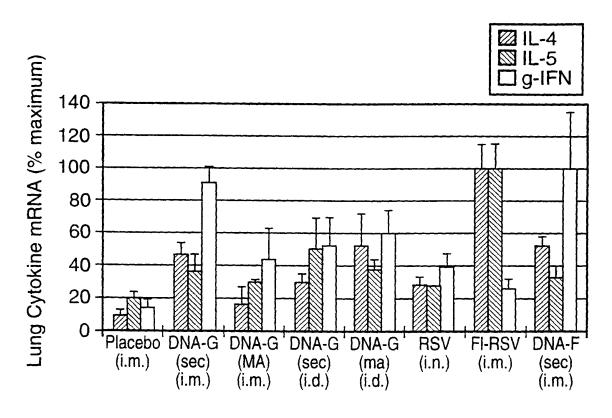


FIG.8